REMARKS

Applicants have amended claims 32 and 39 to include embodiments for identifying single nucleotide polymorphisms (SNPs) in the genome of mammals of the same species. These embodiments derive from Applicants' discovery of the distribution and density of SNPs in a mammalian genome and their penetrating insight that combining SNPs would provide valuable genetic information. Applicants, in their specification, teach and enable the advantageous properties of SNPs for genetic analysis in, among other things, mammals. See the specification, for example, at pages 13-15, page 44, lines 29-36 and Examples 1-6. Moreover, Applicants teach and enable using the combinations of SNPs, even at high allelic frequencies, to provide highly accurate genetic analysis. See the specification, for example, at pages 38-42, Examples 1-6 and Figures 4 and 5.

Applicants have also added new claims 56-58, which include parentage testing that the Examiner implicitly suggests meets the written description requirement. (See Final Office Action, Item 12) Support for new claims 56-58 can be found, for example, at page 37, lines 18-25, pages 41-43 and 47, original claim 12, and Examples 1, 2 and 4. No new matter has been added. Applicants respectfully request entry of this amendment and reconsideration of the application.

Objection to the Specification

The Examiner has objected to the specification for failing to indicate the status of certain applications and for certain documents improperly incorporated by reference into the specification. Applicants respectfully disagree with the Examiner's position. Nevertheless, Applicants have amended the specification to include the status of the application and remove the alleged improper incorporation by reference of certain documents. Applicants respectfully submit that the Examiner's objection is moot in light of the amendments to the specification.

Rejection under 35 U.S.C. §112, First Paragraph: Written Description

The Examiner rejected claims 32-45 under 35 U.S.C. §112, first paragraph for allegedly failing to comply with the written description requirement. Applicants respectfully traverse this rejection.

The Examiner asserts that the specification does not provide adequate written description for identifying single nucleotide polymorphisms in myriad of "species of interests", which includes all life forms including viruses. The Examiner acknowledges that the specification does provide several examples directed to equine and horse DNA. However, the Examiner concludes that there is no written description for the myriad of claimed species of interest.

Applicants respectfully disagree with this rejection, but have amended claims 32-45 in order to expedite prosecution to include methods for identifying single nucleotide polymorphic sites in the genome of mammals of **the same species**.

Applicants submit the specification provides written description and fully enables the claims. The specification at pages 13-15, page 44, lines 29-36 and Examples 1-6 clearly discloses and enables conducting genetic analysis using SNPs from mammalian DNA. Applicants submit that genomic DNA is genomic DNA regardless of the species. Thus, DNA does not chemically vary between species and the analysis of SNPs should not in any way depend on the source of the nucleic acid molecules.

To provide further support, Applicants performed a limited sequence search for mammals other than horses using NIH BLAST search for exact matches of some of the sequences described in Table I of the specification: Sequences ID Nos. 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 25, 45, and 71. Exact matches were found for mammals other than horses, for example in humans, chimpanzees, mice, rat, cow, ring-tailed lemurs and opossums. The BLAST results are listed below.

SEQ ID NO	BLAST MATCH	SPECIES
1 (C Allele)	gi|19852154|gb|AC023315.4| Homo sapiens chromosome 17, clone RP11-333J10, complete sequence Length = 135692 Score = 34.2 bits (17), Expect = 2.1 Identities = 17/17 (100%) Strand = Plus / Minus Query: 5 ctctaagtgctgtgggc 21 ||||||||||||||||| Sbjct:117900 ctctaagtgctgtgggc 117884	Human
1 (T Allele)	gi|31194043|gb|AC129322.3| Mus musculus BAC clone RP23-220F4 from chromosome 19, complete sequence Length = 182093 Score = 32.2 bits (16), Expect = 8.3 Identities = 19/20 (95%) Strand = Plus / Minus Query: 2 cagctctaagtgctgtgggt 21 |||||||||||||||||||| Sbjct: 88019 cagctctaagtgcagtgggt 88000	House Mouse
1 (T Allele)	gi|25815276|gb|AC069513.28| Homo sapiens 3 BAC RP11-171N2 (Roswell Park Cancer Institute Human BAC Library) complete sequence Length = 174097 Score = 32.2 bits (16), Expect = 8.3 Identities = 16/16 (100%) Strand = Plus / Minus Query: 6 tctaagtgctgtgggt 21 |||||||||||||||| Sbjct: 22999 tctaagtgctgtgggt 22984	Human
3 (G Allele)	gi|39725895|gb|AC147117.2| Pan troglodytes BAC clone CH251-532B3 from Y, complete sequence Length = 207020 Score = 34.2 bits (17), Expect = 2.1 Identities = 17/17 (100%) Strand = Plus / Plus Query: 5 ccttagaatttctgcag 21 ||||||||||||||||| Sbjct: 58093 ccttagaatttctgcag 58109	Chimpanzee

3 (G Allele)	gi|56236323|gb|AC145551.5| Mus musculus chromosome UNKNOWN clone RP23-73014, complete sequence
	                    Length = 204610
	
	 Score = 34.2 bits (17), Expect = 2.1
	 Identities = 17/17 (100%)
	 Strand = Plus / Plus
	
	 Query: 5 ccttagaatttctgcag 21
	                |||||||||||||||||
	 Sbjct: 77512 ccttagaatttctgcag 77528
		Mouse

3 (G Allele)	gi|11322840|emb|AL359641.10| Human DNA sequence from clone RP11-402K9 on chromosome Xq21.32-22.2 Contains a novel pseudogene and a laminin receptor 1 (ribosomal protein SA,67kDa) (LAMR1) pseudogene, complete sequence Length = 175132 Score = 34.2 bits (17), Expect = 2.1 Identities = 17/17 (100%) Strand = Plus / Plus Query: 5 ccttagaatttctgcag 21 ||||||||||||||||| Sbjct: 86069 ccttagaatttctgcag 86085	Human
3 (A Allele)	gi|38044276|gb|AC146159.2| Pan troglodytes BAC clone RP43-36O19 from 7, complete sequence Length = 163991 Score = 34.2 bits (17), Expect = 2.1 Identities = 17/17 (100%) Strand = Plus / Minus Query: 5 ccttagaatttctgcaa 21 ||||||||||||||||| Sbjct: 49782 ccttagaatttctgcaa 49766	Chimpanzee
3 (A Allele)	gi|5540113|gb|AC008080.1|AC008080 Homo sapiens clone RP11-89N17 from 7p14-15, complete sequence Length = 178635 Score = 34.2 bits (17), Expect = 2.1 Identities = 17/17 (100%) Strand = Plus / Minus Query: 5 ccttagaatttctgcaa 21 ||||||||||||||||| Sbjct: 53541 ccttagaatttctgcaa 53525	Human

3 (A Allele)	gi|58801546|ref|NM_001003166.1| Canis familiaris CE8 protein, variant 2 (CE8), mRNA Length = 789 Score = 34.2 bits (17), Expect = 2.1 Identities = 17/17 (100%) Strand = Plus / Plus Query: 5 ccttagaatttctgcaa 21 ||||||||||||||||| Sbjct: 397 ccttagaatttctgcaa 413	Human
3 (A Allele)	gi|59709517|gb|AC112984.21| Mus musculus chromosome 18, clone RP24-185P1, complete sequence Length = 171822 Score = 32.2 bits (16), Expect = 8.3 Identities = 16/16 (100%) Strand = Plus / Plus Query: 6 cttagaatttctgcaa 21 |||||||||||||||| Sbjct: 93726 cttagaatttctgcaa 93741	House Mouse

5 (A Allele)	gi|29294367|gb|AC130203.4| Mus musculus BAC clone RP24-413E20 from chromosome 15, complete sequence
	        Length = 182040
	
	Score = 34.2 bits (17), Expect = 2.1
	Identities = 17/17 (100%)
	Strand = Plus / Minus
	
	Query: 1 agctctgggatgatcca 17
	               |||||||||||||||||
	Sbjct: 79633 agctctgggatgatcca 79617
		House Mouse

5 (A Allele)	gi|62000729|gb|AC153981.5| Mus musculus 10 BAC RP24-112H16 (Roswell Park Cancer Institute (C57BL/6J
	              Male) Mouse BAC Library) complete sequence
	Length = 177129
	Score = 34.2 bits (17), Expect = 2.1
	Identities = 17/17 (100%)
	Strand = Plus / Minus
	
	Query: 5 ctgggatgatccactaa 21
	               |||||||||||||||||
	Sbjct: 166294 ctgggatgatccactaa 166278
		House Mouse

5	gi|21217841|emb|AL691483.10| Human DNA	Human

(A Allele)	sequence from clone RP11-484M14 on chromosome 1, complete sequence Length = 90642 Score = 32.2 bits (16), Expect = 8.3 Identities = 16/16 (100%) Strand = Plus / Plus Query: 6 tgggatgatccactaa 21 |||||||||||||||| Sbjct: 32700 tgggatgatccactaa 32715	
7 (T Allele)	gi|21844648|gb|AC115305.4| Mus musculus BAC clone RP24-372L1 from 18, complete sequence Length = 155389 Score = 34.2 bits (17), Expect = 2.1 Identities = 17/17 (100%) Strand = Plus / Plus Query: 5 catcatttttccctcat 21 ||||||||||||||||| Sbjct: 142213 catcatttttccctcat 142229	House Mouse
7 (T Allele)	gi|22138730|emb|AL590556.20| Human DNA sequence from clone RP11-26H16 on chromosome 1 Contains a ribosomal protein L21 (RPL21) pseudogene, the 5' end of the HSPG2 gene for heparan sulfate proteoglycan 2 (perlecan), the ELA3B gene for elastase 3B (pancreatic) and the ELA3A gene for elastase 3A (pancreatic (protease E)), complete sequence Length = 118495 Score = 34.2 bits (17), Expect = 2.1 Identities = 17/17 (100%) Strand = Plus / Minus Query: 5 catcatttttccctcat 21 ||||||||||||||||| Sbjct: 93452 catcatttttccctcat 93436	Human
7 (C Allele)	gi|23462914|gb|AC123044.4| Mus musculus BAC clone RP24-548B7 from chromosome 5, complete sequence Length = 184772 Score = 32.2 bits (16), Expect = 8.3 Identities = 16/16 (100%) Strand = Plus / Plus	House Mouse

	Query: 6 atcatttttccctcac 21 |||||||||||||||| Sbjct: 24180 atcatttttccctcac 24195	
7 (C Allele)	gi|23462914|gb|AC123044.4| Mus musculus BAC clone RP24-548B7 from chromosome 5, complete sequence Length = 184772 Score = 32.2 bits (16), Expect = 8.3 Identities = 16/16 (100%) Strand = Plus / Plus Query: 6 atcatttttccctcac 21 |||||||||||||||| Sbjct: 24180 atcatttttccctcac 24195	House Mouse
7 (C Allele)	gi|18857856|emb|Z98744.2|HS193B12 Human DNA sequence from clone RP1-193B12 on chromosome 6p21.3-22.3 Contains the H2AFD, H2BFD, H2AFI, H1F5, H3FF, H4FK, H3FJ, H2AFN, and H2BFN histone genes, the OR2B2 gene for olfactory receptor 2B2, histone H2B family member I pseudogene H2BFIP, a hypothetical protein pseudogene, ESTs, STSs, GSSs and CpG islands, complete sequence Length = 100374 Score = 34.2 bits (17), Expect = 2.1 Identities = 17/17 (100%) Strand = Plus / Plus Query: 5 catcatttttccctcac 21 ||||||||||||||||| Sbjct: 11160 catcatttttccctcac 11176	Human
9 (G Allele)	gi|21738604|emb|AL731817.11| Mouse DNA sequence from clone RP23-3J16 on chromosome 11 Contains a novel gene and the 3' end of a novel gene, complete sequence Length = 103582 Score = 38.2 bits (19), Expect = 0.14 Identities = 19/19 (100%) Strand = Plus / Minus Query: 3 aactaatttgatggccatg 21 ||||||||||||||||||| Sbjct: 6142 aactaatttgatggccatg 6124	House Mouse

9 (A Allele)	gi|28971516|emb|AL929426.8| Mouse DNA sequence from clone RP23-471H23 on chromosome 11 Contains the 3' end of the Scpep1 gene for serine carboxypeptidase 1, complete sequence Length = 52369 Score = 34.2 bits (17), Expect = 2.1 Identities = 17/17 (100%) Strand = Plus / Minus Query: 5 ctaatttgatggccata 21 ||||||||||||||||| Sbjct: 1959 ctaatttgatggccata 1943	House Mouse
9 (A Allele)	gi|28564367|emb|AL954650.8| Human DNA sequence from clone RP11-523M19 on chromosome 1, complete sequence Length = 86257 Score = 32.2 bits (16), Expect = 8.3 Identities = 16/16 (100%) Strand = Plus / Minus Query: 6 taatttgatggccata 21 |||||||||||||||| Sbjct: 51843 taatttgatggccata 51828	Human
11 (C Allele)	gi|21913039|gb|AC079111.7| Homo sapiens chromosome 17, clone RP11-367G9, complete· sequence Length = 163410 Score = 36.2 bits (18), Expect = 0.53 Identities = 18/18 (100%) Strand = Plus / Minus Query: 4 atcattgttctgactttc 21 |||||||||||||||||| Sbjct: 110475 atcattgttctgactttc 110458	Human
11 (C Allele)	>gi|37719158|gb|AC105075.6| Mus musculus chromosome 1, clone RP23-366P11, complete sequence Length = 195511 Score = 34.2 bits (17), Expect = 2.1 Identities = 17/17 (100%) Strand = Plus / Minus Query: 5 tcattgttctgactttc 21 ||||||||||||||||| Sbjct: 127117 tcattgttctgactttc 127101	House Mouse

11 (T Allele)	gi|6624738|emb|AL049553.20|HSJ402N21 Human DNA sequence from clone RP3-402N21 on chromosome 6p21.1-21.31 Contains the MDGA1 gene for MAM domain containing glycosylphosphatidylinositol anchor 1, the gene for a novel protein and four CpG islands, complete sequence Length = 170302 Score = 42.1 bits (21), Expect = 0.009 Identities = 21/21 (100%) Strand = Plus / Minus Query: 1 gcaatcattgttctgactttt 21 ||||||||||||||||||||| Sbjct: 80929 gcaatcattgttctgactttt 80909	Human
13 (T Allele)	gi|15638795|gb|AC092622.2| Homo sapiens BAC clone RP11-254O14 from 2, complete sequence Length = 19531 Score = 32.2 bits (16), Expect = 8.3 Identities = 16/16 (100%) Strand = Plus / Minus Query: 6 ggcccaagaacaggat 21 |||||||||||||||| Sbjct: 9433 ggcccaagaacaggat 9418	Human
13 (C Allele)	gi|15209313|emb|AL160398.27| Human DNA sequence from clone RP11-15N12 on chromosome 6 Contains the 5' end of the gene for the possible ortholog of R. norvegicus ion transporter protein (NRITP), complete sequence Length = 134995 Score = 32.2 bits (16), Expect = 8.3 Identities = 16/16 (100%) Strand = Plus / Minus Query: 6 ggcccaagaacaggac 21 |||||||||||||||| Sbjct: 94841 ggcccaagaacaggac 94826	Human
13 (C Allele)	gi|16944094|emb|AL583889.8| Mouse DNA sequence from clone RP23-10K12 on chromosome 15, complete sequence Length = 236344 Score = 32.2 bits (16), Expect = 8.3	House Mouse

	Identities = 16/16 (100%) Strand = Plus / Minus Query: 6 ggcccaagaacaggac 21 |||||||||||||||| Sbjct: 78958 ggcccaagaacaggac 78943	
15 (A Allele)	gi|16973887|emb|AL512626.8| Human DNA sequence from clone RP11-163I12 on chromosome 1 Contains part of the ESRRG gene for estrogen-related receptor gamma, complete sequence Length = 106859 Score = 32.2 bits (16), Expect = 8.3 Identities = 19/20 (95%) Strand = Plus / Minus Query: 2 ctgacactcgctgaactcaa 21 |||||||||||||||||||| Sbjct: 17052 ctgacactctctgaactcaa 17033	Human
15 (A Allele)	gi|23820923|gb|AC122270.4| Mus musculus BAC clone RP23-220N16 from 17, complete sequence Length = 196395 Score = 30.2 bits (15), Expect = 33 Identities = 15/15 (100%) Strand = Plus / Minus Query: 7 actcgctgaactcaa 21 ||||||||||||||| Sbjct: 64658 actcgctgaactcaa 64644	House Mouse
15 (A Allele)	gi|62543315|gb|AC123544.4| Lemur catta clone LB2-246N5, complete sequence Length = 195323 Score = 30.2 bits (15), Expect = 33 Identities = 18/19 (94%) Strand = Plus / Minus Query: 3 tgacactcgctgaactcaa 21 ||||||||||||||||||| Sbjct: 1362 tgacaatcgctgaactcaa 1344	Ring- tailed Lemur
15 (G Allele)	gi|60418190|gb|AC108828.17| Mus musculus chromosome 5, clone RP23-153H17, complete sequence Length = 218103 Score = 34.2 bits (17), Expect = 2.1 Identities = 17/17 (100%) Strand = Plus / Minus	House Mouse

	Query: 5 acactcgctgaactcag 21 ||||||||||||||||| Sbjct: 146785 acactcgctgaactcag 146769	
15 (G Allele)	gi|22002199|gb|AC099787.2| Homo sapiens chromosome 1 clone RP4-538N4, complete sequence Length = 177329 Score = 32.2 bits (16), Expect = 8.3 Identities = 16/16 (100%) Strand = Plus / Plus Query: 6 cactcgctgaactcag 21 |||||||||||||||| Sbjct: 61135 cactcgctgaactcag 61150	Human
17 (T Allele)	gi|30409940|gb|AC123056.4| Mus musculus BAC clone RP23-182H4 from chromosome 13, complete sequence Length = 183076 Score = 36.2 bits (18), Expect = 0.53 Identities = 18/18 (100%) Strand = Plus / Plus Query: 4 gaaagaccacattatttt 21 |||||||||||||||||| Sbjct: 86528 gaaagaccacattatttt 86545	House Mouse
17 (T Allele)	gi|2791551|emb|AL008725.1|HS148E22 Human DNA sequence from clone RP1-148E22 on chromosome 20q12-13.12 Contains the YWHAB gene encoding tyrosine 3-monooxygenase/ntryptophan 5- monooxygenase activation protein, beta polypeptide, a novel gene similar to PABPC1 (poly (A)-binding protein, cytoplasmic 1), 2 CpG islands, ESTs, STSs and GSSs, complete sequence Length = 79227 Score = 34.2 bits (17), Expect = 2.1 Identities = 17/17 (100%) Strand = Plus / Minus Query: 5 aaagaccacattatttt 21 ||||||||||||||||| Sbjct: 15937 aaagaccacattatttt 15921	Human
17 (T Allele)	gi|31044300|gb|AC129066.3| Didelphis virginiana clone LB3-8N21, complete sequence Length = 158526 Score = 34.2 bits (17), Expect = 2.1	North American Opossum

	Identities = 17/17 (100%) Strand = Plus / Minus Query: 5 aaagaccacattatttt 21 ||||||||||||||||| Sbjct: 52085 aaagaccacattatttt 52069	
17 (T Allele)	gi|29294415|gb|AC142296.1| Pan troglodytes BAC clone RP43-97L1 from Y, complete sequence Length = 158231 Score = 32.2 bits (16), Expect = 8.3 Identities = 16/16 (100%) Strand = Plus / Minus Query: 6 aagaccacattatttt 21 |||||||||||||||| Sbjct: 101310 aagaccacattatttt 101295	Chimpanzee
17 (T Allele)	gi|30270589|gb|AC120570.5| Rattus norvegicus 1 BAC CH230-96N8 (Children's Hospital Oakland Research Institute) complete sequence Length = 227607 Score = 32.2 bits (16), Expect = 8.3 Identities = 16/16 (100%) Strand = Plus / Minus Query: 6 aagaccacattatttt 21 |||||||||||||||| Sbjct: 184656 aagaccacattatttt 184641	Norway Rat
17 (A Allele)	gi|48675476|gb|AC144933.4| Mus musculus BAC clone RP24-531B24 from chromosome 8, complete sequence Length = 169667 Score = 36.2 bits (18), Expect = 0.21 Identities = 18/18 (100%) Strand = Plus / Minus Query: 1 gaaagaccacattattta 18 |||||||||||||||||| Sbjct: 118910 gaaagaccacattattta 118893	House Mouse
17 (A Allele)	gi|11096675|emb|AL356794.10| Human DNA sequence from clone RP11-551A11 on chromosome 6 Contains a ribosomal protein S3A (40S ribosomal protein S3a, v-fos transformation effector protein 1) (RPS3A)(FTE1) pseudogene, complete sequence Length = 164439	Human

	Score = 34.2 bits (17), Expect = 2.1 Identities = 20/21 (95%) Strand = Plus / Minus Query: 1 tgggaaagaccacattattta 21 ||||||||||||||||||||| Sbjct: 142830 tgggaaagaccactttattta 142810	
19 (A Allele)	gi|29823238|emb|AL844164.17| Mouse DNA sequence from clone RP23-300I3 on chromosome 4, complete sequence Length = 209214 Score = 40.1 bits (20), Expect = 0.034 Identities = 20/20 (100%) Strand = Plus / Minus Query: 2 gtctgaaacaaaagggaaca 21 |||||||||||||||||||| Sbjct: 24553 gtctgaaacaaaagggaaca 24534	House Mouse
19 (A Allele)	gi|62123257|gb|AC159375.1| Pan troglodytes chromosome UNKNOWN clone CH251-557H18, complete sequence Length = 184511 Score = 34.2 bits (17), Expect = 2.1 Identities = 17/17 (100%) Strand = Plus / Plus Query: 5 tgaaacaaaagggaaca 21 ||||||||||||||||| Sbjct: 42683 tgaaacaaaagggaaca 42699	Chimpanzee

19
(A Allele)
	gi|20503261|gb|AC115112.5| Homo sapiens
	BAC clone RP11-427M12 from 4, complete
	sequence
	         Length = 142494
	
	Score = 34.2 bits (17), Expect = 2.1
	Identities = 17/17 (100%)
	Strand = Plus / Plus
	
	Query: 5 tgaaacaaaagggaaca 21
	                  |||||||||||||||||
	Sbjct: 117698 tgaaacaaaagggaaca 117714
		Human

19 (T Allele)	gi|20564428|gb|AC073372.9| Homo sapiens chromosome 11 clone RP11-500D4, complete sequence Length = 180504 Score = 38.2 bits (19), Expect = 0.14	Human

	Identities = 19/19 (100%) Strand = Plus / Minus Query: 3 tctgaaacaaaagggaact 21 ||||||||||||||||||| Sbjct: 163198 tctgaaacaaaagggaact 163180	
19 (T Allele)	gi|51241710|emb|AL808125.11| Mouse DNA sequence from clone RP23-193L22 on chromosome 2, complete sequence Length = 236619 Score = 34.2 bits (17), Expect = 2.1 Identities = 17/17 (100%) Strand = Plus / Plus Query: 5 tgaaacaaaagggaact 21 ||||||||||||||||| Sbjct: 28213 tgaaacaaaagggaact 28229	House Mouse
21 (G Allele)	gi|56787768|gb|AC123698.15| Mus musculus chromosome 15, clone RP23-331P14, complete sequence Length = 201739 Score = 32.2 bits (16), Expect = 8.3 Identities = 19/20 (95%) Strand = Plus / Plus Query: 2 atgagtaagaagcatccggg 21 ||||||||||||||||||| Sbjct: 150709 atgagcaagaagcatccggg 150728	House Mouse
71 (C Allele)	gi|20339152|emb|AL670720.7| Mouse DNA sequence from clone RP23-321M9 on chromosome 4, complete sequence Length = 200628 Score = 32.2 bits (16), Expect = 8.3 Identities = 16/16 (100%) Strand = Plus / Plus Query: 6 ccagactattgggacc 21 |||||||||||||||| Sbjct: 102456 ccagactattgggacc 102471	House Mouse
45 (C Allele)	gi|18044094|gb|BC019461.1| Mus musculus DNA segment, Chr 4, Brigham & Women's Genetics 1540 expressed, mRNA (cDNA clone MGC:28642 IMAGE:4224033), complete cds Length = 1461 Score = 38.2 bits (19), Expect = 0.14	House Mouse

	Identities = 19/19 (100%) Strand = Plus / Plus Query: 3 gaacggagagcaggccttc 21 ||||||||||||||||||| Sbjct: 1158 gaacggagagcaggccttc 1176	
45 (G Allele)	gi|28867179|gb|AC123925.4| Mus musculus BAC clone RP24-292N2 from chromosome 15, complete sequence Length = 166696 Score = 34.2 bits (17), Expect = 2.1 Identities = 17/17 (100%) Strand = Plus / Plus Query: 5 acggagagcaggccttg 21 ||||||||||||||||| Sbjct: 8541 acggagagcaggccttg 8557	House Mouse
45 (G Allele)	gi|37790797|gb|AY436323.1| Homo sapiens angiotensinogen (serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 8) (AGT) gene, complete cds Length = 15593 Score = 32.2 bits (16), Expect = 8.3 Identities = 16/16 (100%) Strand = Plus / Plus Query: 6 cggagagcaggccttg 21 |||||||||||||||| Sbjct: 7852 cggagagcaggccttg 7867	Human
25 (C Allele)	gi|5649375|gb|AC007253.2| Homo sapiens BAC clone RP11-454P5 from 2, complete sequence Length = 225699 Score = 32.2 bits (16), Expect = 8.3 Identities = 16/16 (100%) Strand = Plus / Minus Query: 6 gaacaggattgagttc 21 |||||||||||||||| Sbjct: 202335 gaacaggattgagttc 202320	Human
25 (C Allele)	gi|62123195|gb|AC154832.2| Mus musculus chromosome 14 clone RP24-568D4, complete sequence Length = 134900 Score = 32.2 bits (16), Expect = 8.3 Identities = 19/20 (95%)	House Mouse

	Strand = Plus / Minus Query: 2 ccaagaacaggattgagttc 21 ||||||||||||||||||| Sbjct: 1377 ccaaggacaggattgagttc 1358	
25 (T Allele)	gi|62123165|gb|AC123530.4| Mus musculus BAC clone RP24-194D2 from chromosome 10, complete sequence Length = 164420 Score = 36.2 bits (18), Expect = 0.53 Identities = 18/18 (100%) Strand = Plus / Plus Query: 4 aagaacaggattgagttt 21 |||||||||||||||||| Sbjct: 52179 aagaacaggattgagttt 52196	House Mouse

25
(T Allele)
	gi|51699533|gb|AC150516.2| Bos taurus
	BAC CH240-117L9 (Children's Hospital
	Oakland Research
	Institute Bovine BAC Library (male))
	complete sequence
	Length = 237116
	Score = 34.2 bits (17), Expect = 2.1
	Identities = 17/17 (100%)
	Strand = Plus / Plus
	
	Query: 2 ccaagaacaggattgag 18
	             |||||||||||||||||
	Sbjct: 134113 ccaagaacaggattgag 134129
	Score = 26.3 bits (13), Expect = 514
	Identities = 13/13 (100%)
	Strand = Plus / Minus
	
	Query: 9 caggattgagttt 21
	             |||||||||||||
	Sbjct: 178822 caggattgagttt 178810
		Cow

25 (T Allele)	gi|13435286|gb|AC019211.6| Homo sapiens BAC clone RP11-454J11 from 2, complete sequence Length = 167471 Score = 32.2 bits (16), Expect = 8.3 Identities = 16/16 (100%) Strand = Plus / Minus Query: 6 gaacaggattgagttt 21 |||||||||||||||| Sbjct: 48760 gaacaggattgagttt 48745	Human

Clearly, if these sequences are present in horse, they can be and indeed were identified in other species of interest.

Moreover, the amended and new claims are directed to use of SNPs in genetic analysis of genomic DNA obtained from mammals of **the same species**. The application as filed satisfies the written description requirement because it unambiguously conveys to those of skill in the art that the Applicant was in possession of the claimed invention as of the priority date. Applicants' insight that combinations of SNPs would be extremely useful as genetic markers and can be used for genetic analysis follows from their discovery regarding the distribution and density of SNPs in mammalian genomes. While the illustrative examples in the specification are directed to horse and human studies, one or ordinary skill in the art upon reading the specification would readily understand that the methods and use of SNPs would be applicable to all species including mammals. Applicants have described this applicability throughout their specification. This is further demonstrated by the limited BLAST sequence comparison conducted, which identifies the same SNPs that are found in horses are found in humans, chimpanzees, mice, ring-tailed lemurs, rats, cows and opossums. Therefore, it is respectfully submitted that the specification fully complies with the written description requirement for methods of identifying single nucleotide polymorphic sites in the genome of mammals of the same species. Accordingly, Applicants respectfully request withdrawal of this rejection.

Rejections Under 35 U.S.C. § 112, First Paragraph: Enablement

The Examiner rejected claims 32-45 under 35 U.S.C. §112, first paragraph for allegedly failing to comply with the enablement requirement. Applicants respectfully traverse this rejection.

While the Examiner asserts that the specification does present several examples directed to the analysis of equine and human DNA, the Examiner concludes that the six examples do not enable identification of mutations in any or all mammalian species.

Applicants respectfully disagree with this rejection, but have amended claims 32-45 in order to expedite prosecution to include methods for identifying single nucleotide polymorphic sites in the genome of mammals of the same species.

Applicants submit that genomic DNA is genomic DNA regardless of the species and DNA does not chemically vary between species. It follows that the analysis of SNPs should not in any way depend on the source of the nucleic acid molecules. As stated above, Applicants performed a limited sequence search for mammals other than horses using NIH BLAST search for exact matches of some of the sequences described in Table I of the specification: Sequences ID Nos. 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 25, 45, and 71. Exact matches were found for mammals other than horses, for example in humans, chimpanzees, mice, rats, cows, ring-tailed lemurs and opossums. Moreover, Applicants are not claiming individual SNPs, but methods using the combinations of SNPs as useful genetic markers to provide valuable genetic information.

The Examiner's reliance on *Genentech v. Novo Nordisk* (*"Genentech"*) as analogous to the present case is misplaced. *Genentech* was decided on strikingly different facts. In *Genentech*, the claims recited a method for making human growth hormone in a fusion protein and cleaving the fusion protein to make the growth hormone. The patentees in *Genentech* tried to rely on the level of skill in the art to enable the claim, but at the time of filing the application it was *not* known in the art how to cleave a fusion protein to make growth hormone, *where the cleaving of the fusion protein was the novel aspect of the claim*. In contrast, the novel aspect of the amended claims does not include claims to individual SNPs, but methods using the combinations of SNPs as useful genetic markers. Thus, *Genentech* sheds no light on any alleged written description or enablement issues with respect to the present claims. *Genentech* is simply inapplicable to the facts of this case.

It is respectfully submitted that the specification fully complies with the enablement requirement for methods of identifying single nucleotide polymorphic sites in the genome of mammals of the same species. Accordingly, Applicants respectfully request withdrawal of this rejection.

Conclusion

Reconsideration and allowance are respectfully solicited.

Enclosed is the fee for a three-month extension of time and fee for filing a

Request For Continued Examination. No additional fee is believed to be due with respect

to the filing of this amendment. If any additional fees are due, or an overpayment has

been made, please charge, or credit, our Deposit Account No. 11-0171 for such sum.

If the Examiner has any questions regarding the present application, the Examiner

is cordially invited to contact Applicant's attorney at the telephone number provided

below.

Respectfully submitted,

William D. Schmidt
Registration No.: 39,492
Attorney for Applicant

Kalow & Springut LLP
Telephone No.: (212) 813-1600